```
Database :        UniProt_03:*
                  1:   uniprot_sprot:*
                  2:   uniprot_trembl:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.


                                    SUMMARIES
                  %
Result            Query
  No.    Score  Match Length DB  ID                    Description
----------------------------------------------------------------------------
     1    925   54.2    322   1  ALDX_SPOSA            P27800 sporobolomy
     2    658   38.5    315   2  Q9AW93                Q9aw93 digitalis p
     3    654   38.3    323   2  Q6C177                Q6c177 yarrowia li
     4    653   38.2    315   2  Q9AW92                Q9aw92 digitalis p
     5   651.5  38.1    316   2  Q9VTK9                Q9vtk9 drosophila
     6   648.5  38.0    324   1  AKA1_RAT              P51635 rattus norv
     7    647   37.9    312   1  GCY_YEAST             P14065 saccharomyc
     8   640.5  37.5    324   1  AKA1_MOUSE            Q9jii6 mus musculu
     9   640.5  37.5    325   2  Q80XJ7                Q80xj7 mus musculu
    10   639.5  37.4    313   2  O82020                O82020 medicago sa
    11    638   37.4    350   2  Q8IQF8                Q8iqf8 drosophila
    12   636.5  37.3    324   1  AKA1_PIG              P50578 sus scrofa
    13   635.5  37.2    324   1  AKA1_HUMAN            P14550 homo sapien
    14    634   37.1    327   2  P74308                P74308 synechocyst
    15   631.5  37.0    324   2  Q6AZW2                Q6azw2 brachydanio
    16   631.5  37.0    327   2  Q6GMC7                Q6gmc7 xenopus lae
    17    627   36.7    290   2  O80945                O80945 arabidopsis
    18    623   36.5    314   2  Q84TF0                Q84tf0 arabidopsis
    19   621.5  36.4    311   2  Q941T6                Q941t6 oryza sativ
    20   621.5  36.4    350   2  Q7XJP3                Q7xjp3 arabidopsis
    21    620   36.3    312   1  YPR1_YEAST            Q12458 saccharomyc
    22    618   36.2    304   2  Q84W94                Q84w94 arabidopsis
    23   616.5  36.1    327   2  Q6AZC3                Q6azc3 brachydanio
    24   614.5  36.0    311   2  Q941T8                Q941t8 oryza sativ
```

```
Database :        PIR_79:*
                  1:  pirl:*
                  2:  pir2:*
                  3:  pir3:*
                  4:  pir4:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	925	54.2	323	2	S78113	aldehyde reductase
2	648.5	38.0	325	1	JN0629	alcohol dehydrogen
3	647	37.9	312	1	S22846	probable aldehyde
4	639.5	37.4	313	2	T09670	abscisic acid acti
5	635.5	37.2	325	2	A33851	alcohol dehydrogen
6	634	37.1	327	1	S76143	probable aldehyde
7	627	36.7	290	2	T02543	aldehyde dehydroge
8	621.5	36.4	350	2	B84797	probable alcohol d
9	620	36.3	312	2	S61163	aldo-keto reductas
10	610.5	35.7	316	2	T26766	hypothetical prote
11	609	35.7	315	2	T45928	reductase-like pro
12	603.5	35.3	321	2	T38413	probable oxidoredu
13	599.5	35.1	316	1	A60603	aldehyde reductase
14	591.5	34.6	316	1	A39763	aldehyde reductase
15	585.5	34.3	315	1	A35452	aldehyde reductase
16	585.5	34.3	316	2	I49484	aldehyde reductase
17	575.5	33.7	316	2	A59021	aldehyde reductase
18	573.5	33.6	323	2	JC5240	3alpha-hydroxychol
19	573	33.5	294	2	T02542	probable alcohol d

```
Database :        Published_Applications_AA:*
                  1:  /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
                  2:  /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
                  3:  /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
                  4:  /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
                  5:  /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
                  6:  /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
                  7:  /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
                  8:  /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
                  9:  /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
                  10:  /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
                  11:  /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
                  12:  /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
                  13:  /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
                  14:  /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
                  15:  /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
                  16:  /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
                  17:  /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
                  18:  /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
                  19:  /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
                  20:  /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1708	100.0	328	13	US-10-040-416-4	Sequence 4, Appli
2	1697	99.4	328	13	US-10-040-416-6	Sequence 6, Appli
3	1495	87.5	330	9	US-09-800-487A-2	Sequence 2, Appli
4	1495	87.5	330	13	US-10-040-416-2	Sequence 2, Appli
5	906.5	53.1	322	10	US-09-734-237B-32	Sequence 32, Appl
6	684.5	40.1	356	15	US-10-369-493-13122	Sequence 13122, A
7	673.5	39.4	313	15	US-10-424-599-221377	Sequence 221377,
8	668	39.1	313	15	US-10-424-599-282510	Sequence 282510,
9	660	38.6	314	15	US-10-424-599-144593	Sequence 144593,
10	656	38.4	298	15	US-10-369-493-13144	Sequence 13144, A
11	650	38.1	313	10	US-09-882-691-6	Sequence 6, Appli
12	650	38.1	313	15	US-10-424-599-221378	Sequence 221378,
13	648.5	38.0	325	16	US-10-472-317-36	Sequence 36, Appl
14	647	37.9	312	10	US-09-734-237B-42	Sequence 42, Appl
15	647	37.9	312	15	US-10-369-493-22372	Sequence 22372, A

```
Database :        Issued_Patents_AA:*
                  1:  /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
                  2:  /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
                  3:  /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
                  4:  /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
                  5:  /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                  6:  /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	906.5	53.1	322	4	US-09-734-237B-32	Sequence 32, Appl
2	650	38.1	313	3	US-09-347-803-6	Sequence 6, Appli
3	647	37.9	312	4	US-09-734-237B-42	Sequence 42, Appl
4	647	37.9	313	4	US-09-734-237B-44	Sequence 44, Appl
5	639.5	37.4	313	3	US-09-347-803-25	Sequence 25, Appl
6	620	36.3	313	4	US-09-734-237B-39	Sequence 39, Appl
7	608.5	35.6	308	3	US-09-347-803-8	Sequence 8, Appli
8	600.5	35.2	302	4	US-09-270-767-45294	Sequence 45294, A
9	599.5	35.1	316	3	US-08-801-344-4	Sequence 4, Appli
10	599.5	35.1	316	3	US-09-498-599-4	Sequence 4, Appli
11	584	34.2	290	4	US-09-248-796A-17316	Sequence 17316, A
12	574.5	33.6	316	1	US-08-585-595-3	Sequence 3, Appli

```
Database :        A_Geneseq_16Dec04:*
                  1:  geneseqp1980s:*
                  2:  geneseqp1990s:*
                  3:  geneseqp2000s:*
                  4:  geneseqp2001s:*
                  5:  geneseqp2002s:*
                  6:  geneseqp2003as:*
                  7:  geneseqp2003bs:*
                  8:  geneseqp2004s:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1708	100.0	328	5	ABP53551	Abp53551 T. megach
2	1697	99.4	328	5	ABP53552	Abp53552 T. megach
3	1495	87.5	330	5	ABP53550	Abp53550 T. megach
4	925	54.2	323	2	AAR96294	Aar96294 Carbonyl
5	906.5	53.1	322	4	AAG63561	Aag63561 Amino aci
6	684.5	40.1	356	8	ADS24089	Ads24089 Bacterial
7	656	38.4	298	8	ADS24111	Ads24111 Bacterial
8	650	38.1	313	4	AAB47466	Aab47466 G. max al
9	650	38.1	313	7	AAE39522	Aae39522 Soybean a
10	648.5	38.0	325	5	ABP53620	Abp53620 Glucurona
11	648.5	38.0	325	8	ADF42772	Adf42772 Rat aldeh
12	648	37.9	312	2	AAW29218	Aaw29218 S. cerevi
13	647.5	37.9	313	2	AAY06231	Aay06231 Alfalfa a

```
Database :        EST:*
                  1:  gb_est1:*
                  2:  gb_est2:*
                  3:  gb_htc:*
                  4:  gb_est3:*
                  5:  gb_est4:*
                  6:  gb_est5:*
                  7:  gb_est6:*
                  8:  gb_gss1:*
                  9:  gb_gss2:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	234.8	21.8	790	7	CF642818	CF642818 D56_C10 F
2	225	20.9	706	7	CF644498	CF644498 K21_H01 F
3	206.6	19.2	1061	4	BI948347	BI948347 HVSME1000
4	186	17.3	585	7	CF638990	CF638990 D09_H04 F
5	184	17.1	556	6	CD489982	CD489982 T30_H09 T
6	184	17.1	619	7	CF643073	CF643073 D59_D08 F
7	183	17.0	551	7	CF639302	CF639302 D13_H10 F
8	179.8	16.7	547	7	CV096678	CV096678 FAMU_USDA
9	179.4	16.7	684	7	CK447487	CK447487 N1A12.SP6
10	169.2	15.7	687	7	CK447233	CK447233 N7C2.SP6
11	167.6	15.6	626	6	CD488246	CD488246 T06_E03 T
12	163.6	15.2	779	1	AA263299	AA263299 LD06393.5
13	163.4	15.2	510	7	CF639847	CF639847 D20_D06 F
14	162.6	15.1	758	1	AA697426	AA697426 HL02448.5
15	161.8	15.0	477	7	CF640529	CF640529 D28_D04 F
16	161.4	15.0	638	6	CA015279	CA015279 HT13N05r
17	160.8	14.9	769	7	CF869025	CF869025 tric017xh
18	160.8	14.9	823	6	CB899137	CB899137 tric017xh
19	160.4	14.9	746	7	CV528275	CV528275 dba59b08.
20	159.6	14.8	384	7	CF640582	CF640582 D28_H11 F

```
Database :          Published_Applications_NA:*
                1:  /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
                2:  /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                3:  /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
                4:  /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
                5:  /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                6:  /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
                7:  /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
                8:  /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
                9:  /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
               10:  /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
               11:  /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
               12:  /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
               13:  /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
               14:  /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
               15:  /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
               16:  /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
               17:  /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
               18:  /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
               19:  /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
               20:  /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
               21:  /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
               22:  /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1077	100.0	1077	13	US-10-040-416-3	Sequence 3, Appli
2	1040.2	96.6	1121	13	US-10-040-416-5	Sequence 5, Appli
3	613.4	57.0	1119	9	US-09-800-487A-1	Sequence 1, Appli
4	613.4	57.0	1119	13	US-10-040-416-1	Sequence 1, Appli
5	315.4	29.3	972	10	US-09-734-237B-31	Sequence 31, Appl
6	279.4	25.9	972	10	US-09-734-237B-33	Sequence 33, Appl

```
Database :        Issued_Patents_NA:*
                  1:  /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
                  2:  /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
                  3:  /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                  4:  /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                  5:  /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                  6:  /cgn2_6/ptodata/1/ina/backfiles1.seq:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	315.4	29.3	972	4	US-09-734-237B-31	Sequence 31, Appl
2	279.4	25.9	972	4	US-09-734-237B-33	Sequence 33, Appl
3	155.6	14.4	954	2	US-08-336-198C-2	Sequence 2, Appli
4	155.6	14.4	954	4	US-09-184-965-2	Sequence 2, Appli
5	154.2	14.3	1290	4	US-09-270-767-13724	Sequence 13724, A
6	148.8	13.8	1073	3	US-09-347-803-5	Sequence 5, Appli
7	143.2	13.3	1512	4	US-09-270-767-15148	Sequence 15148, A
8	143	13.3	1337	3	US-08-801-344-3	Sequence 3, Appli
9	143	13.3	1337	3	US-09-498-599-3	Sequence 3, Appli
10	136	12.6	1132	4	US-09-626-002-18	Sequence 18, Appl
11	128.4	11.9	1335	4	US-09-023-655-1010	Sequence 1010, Ap
12	124	11.5	1196	4	US-09-626-002-17	Sequence 17, Appl
13	121.6	11.3	942	4	US-09-734-237B-43	Sequence 43, Appl
14	117	10.9	942	4	US-09-734-237B-40	Sequence 40, Appl

```
Database :        N_Geneseq_16Dec04:*
                  1:   geneseqn1980s:*
                  2:   geneseqn1990s:*
                  3:   geneseqn2000s:*
                  4:   geneseqn2001as:*
                  5:   geneseqn2001bs:*
                  6:   geneseqn2002as:*
                  7:   geneseqn2002bs:*
                  8:   geneseqn2003as:*
                  9:   geneseqn2003bs:*
                  10:  geneseqn2003cs:*
                  11:  geneseqn2003ds:*
                  12:  geneseqn2004as:*
                  13:  geneseqn2004bs:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

<div align="center">SUMMARIES</div>

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1077	100.0	1077	6	ABQ82226	Abq82226 T. megach
2	1040.2	96.6	1121	6	ABQ82227	Abq82227 T. megach
3	613.4	57.0	1119	6	ABQ82225	Abq82225 T. megach
4	315.4	29.3	972	2	AAT29160	Aat29160 Carbonyl
5	315.4	29.3	972	5	AAH74577	Aah74577 Nucleotid
6	315.4	29.3	1055	2	AAT29159	Aat29159 Carbonyl
7	279.4	25.9	972	5	AAH74578	Aah74578 A synthet
8	180.4	16.8	656	8	ABZ53102	Abz53102 Aspergill
9	163.6	15.2	978	4	ABL10491	Abl10491 Drosophil
10	157.2	14.6	1231	2	AAX58867	Aax58867 Alfalfa a
11	155.6	14.4	954	2	AAQ14352	Aaq14352 Xylose re

```
Database :        GenEmbl:*
                  1:  gb_ba:*
                  2:  gb_htg:*
                  3:  gb_in:*
                  4:  gb_om:*
                  5:  gb_ov:*
                  6:  gb_pat:*
                  7:  gb_ph:*
                  8:  gb_pl:*
                  9:  gb_pr:*
                  10:  gb_ro:*
                  11:  gb_sts:*
                  12:  gb_sy:*
                  13:  gb_un:*
                  14:  gb_vi:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

<div align="center">SUMMARIES</div>

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1077	100.0	1077	6	BD177580	BD177580 Erythrose
2	1077	100.0	1077	6	BD177585	BD177585 Erythrose
3	1077	100.0	1077	6	AX470402	AX470402 Sequence
4	1040.2	96.6	1121	6	BD177581	BD177581 Erythrose
5	1040.2	96.6	1121	6	BD177586	BD177586 Erythrose
6	1040.2	96.6	1121	6	AX470403	AX470403 Sequence
7	613.4	57.0	1119	6	BD177579	BD177579 Erythrose
8	613.4	57.0	1119	6	BD177584	BD177584 Erythrose
9	613.4	57.0	1119	6	AX470401	AX470401 Sequence
10	315.4	29.3	1055	6	E11242	E11242 cDNA encodi
11	170.6	15.8	2309	8	SSU26463	U26463 Sporidiobol
12	163.6	15.2	978	6	CQ585219	CQ585219 Sequence